

## SEQUENCE LISTING

&lt;110&gt; Zankel, et al.

&lt;120&gt; MANUFACTURE OF HIGHLY PHOSPHORYLATED LYSOSOMAL ENZYMES AND USES THEREOF

&lt;130&gt; 30610/39385A

&lt;150&gt; US 60/542,586

&lt;151&gt; 2004-02-06

&lt;160&gt; 4

&lt;170&gt; PatentIn version 3.3

&lt;210&gt; 1

&lt;211&gt; 2847

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 1

```

atgaaagggg cctcctgct gctgctgggt tcaaacctgc tcctgtgcca gagcgggtcc      60
ggagccgggg cccacatcct actccatgat ttctgctgg ttccccgaga gctgagtggc      120
tcctccccag tcctggagga gactcacca gctcaccagc agggagccag cagaccaggg      180
ccccgggatg ccaggcaca ccccggccgt ccagagcag tgcccacaca gtgcgacgtc      240
cccccaaca gccgcttcga ttgcgccct gacaaggcca tcaccagga acagtgcgag      300
gcccgcggt gctgctacat cctgcaaag caggggctgc agggagccca gatggggcag      360
ccctggtgct tcttcccacc cagctacccc agctacaagc tggagaacct gagtcctct      420
gaaatgggt acacggccac cctgaccgt accaccccca cttcttccc caaggacatc      480
ctgaccctgc ggctggacgt gatgatggag actgagaacc gcctccactt cagatcaaa      540
gatccagcta acaggcgcta cgaggtgccc ttggagacct cgctgtcca cagccgggca      600
ccgtccccc tctacagcgt ggagttctcc gaggagccct tcgggggat cgtgcaccgg      660
cagctggacg gccgctgct gctgaacacg acgggtggcg cctgttctt tgcggaccag      720
ttccttcagc tgtccacctc gctgcctcg cagtatatca caggcctcg cgagcacctc      780
agtcccctga tgctcagcac cagctggacc aggatcacc tgtggaaccg ggaccttgcg      840
cccacgccc gtgcgaacct ctacgggtct caccctttct acctggcgct ggaggacggc      900
gggtcggcac acggggtgtt cctgctaaac agcaatgcca tggatgtggt cctgcagccg      960
agccctgccc ttagctggag gtcgacaggt gggatcctgg atgtctacat cttcctgggc      1020
ccagagccca agagcgtggt gcagcagtac ctggacgttg tgggataccc gttcatgccg      1080
ccatactggg gcctgggctt ccacctgtgc cgtggggct actcctccac cgtatcacc      1140
cgccaggtgg tggagaacat gaccagggcc cacttcccc tggacgtcca atggaacgac      1200
ctggactaca tggactccc gagggacttc acgttcaaca aggatggctt ccgggacttc      1260

```

ccggccatgg tgcaggagct gcaccagggc ggccggcgct acatgatgat cgtggatcct	1320
gcatcagca gctcggggccc tgccggggagc tacaggccct acgacgaggg tctgcggagg	1380
gggggttttca tcaccaacga gaccggccag ccgctgattg ggaaggatat gcccgggtcc	1440
actgccttcc ccgacttcac caaccccaca gccctggcct ggtgggagga catggtggct	1500
gagttccatg accaggtgcc cttcgacggc ttgtggattg acatgaacga gccttccaac	1560
ttcatcagag gctctgagga cggtgcccc aacaatgagc tggagaacct accctacgtg	1620
cctgggggtg ttggggggac cctccaggcg gccaccatct gtgcctccag ccaccagttt	1680
ctctccacac actacaacct gcacaacctc tacggcctga ccgaacctat cgcctccac	1740
agggcgctgg tgaaggctcg ggggacacgc ccatttgtga tctcccgctc gacctttgct	1800
ggccacggcc gatacgccgg ccaactggacg ggggacgtgt ggagctcctg ggagcagctc	1860
gcctcctccg tgccagaaat cctgcagttt aacctgctgg gggcgctctt ggtcggggcc	1920
gacgtctgcg gcttcttggg caacacctca gaggagctgt gtgtgcgctg gacctagctg	1980
ggggccttct accccttcat gcggaaccac aacagcctgc tcagtctgcc ccaggagccg	2040
tacagcttca gcgagccggc ccagcaggcc atgaggaagg ccctcacctt gcgctacgca	2100
ctcctccccc acctctacac actgttccac caggccacg tcgcggggga gacctggcc	2160
cggcccctct tcttgagtt ccccaaggac tctagcacct ggactgtgga ccaccagctc	2220
ctgtgggggg aggccttget catcacccca gtgctccagg ccgggaaggc cgaagtgact	2280
ggctacttcc ccttgggcac atggtacgac ctgcagacgg tgccaataga ggcccttggc	2340
agcctccac cccacctgc agctccccgt gagccagcca tccacagcga ggggcagtgg	2400
gtgacgctgc cggccccctt ggacaccatc aacgtccacc tccgggctgg gtacatcatc	2460
cccctgcagg gccctggcct cacaaccaca ggtcccgcc agcagcccat ggccctggct	2520
gtggccctaa ccaaggggtg agaggcccg ggggagctgt tctgggacga tggagagagc	2580
ctggaagtgc tggagcgagg ggcctacaca caggtcatct tctggccag gaataacacg	2640
atcgtgaatg agctggtacg tgtgaccagt gaggagctg gcctgcagct gcagaagggtg	2700
actgtcctgg gcgtggccac ggcgccccag caggtcctct ccaacggtgt ccctgtctcc	2760
aacttcacct acagccccga caccaaggtc ctggacatct gtgtctcgct gttgatggga	2820
gagcagtttc tcgtcagctg gtgttga	2847

<210> 2  
 <211> 948  
 <212> PRT  
 <213> Mus musculus

<400> 2

Met Lys Gly Ser Leu Leu Leu Leu Leu Val Ser Asn Leu Leu Leu Cys

1		5		10		15										
Gln	Ser	Gly	Ser	Gly	Ala	Gly	Ala	His	Ile	Leu	Leu	His	Asp	Phe	Leu	
		20						25					30			
Leu	Val	Pro	Arg	Glu	Leu	Ser	Gly	Ser	Ser	Pro	Val	Leu	Glu	Glu	Thr	
		35					40					45				
His	Pro	Ala	His	Gln	Gln	Gly	Ala	Ser	Arg	Pro	Gly	Pro	Arg	Asp	Ala	
	50					55					60					
Gln	Ala	His	Pro	Gly	Arg	Pro	Arg	Ala	Val	Pro	Thr	Gln	Cys	Asp	Val	
65					70					75					80	
Pro	Pro	Asn	Ser	Arg	Phe	Asp	Cys	Ala	Pro	Asp	Lys	Ala	Ile	Thr	Gln	
				85					90						95	
Glu	Gln	Cys	Glu	Ala	Arg	Gly	Cys	Cys	Tyr	Ile	Pro	Ala	Lys	Gln	Gly	
		100						105					110			
Leu	Gln	Gly	Ala	Gln	Met	Gly	Gln	Pro	Trp	Cys	Phe	Phe	Pro	Pro	Ser	
		115					120					125				
Tyr	Pro	Ser	Tyr	Lys	Leu	Glu	Asn	Leu	Ser	Ser	Ser	Glu	Met	Gly	Tyr	
	130					135					140					
Thr	Ala	Thr	Leu	Thr	Arg	Thr	Thr	Pro	Thr	Phe	Phe	Pro	Lys	Asp	Ile	
145					150					155					160	
Leu	Thr	Leu	Arg	Leu	Asp	Val	Met	Met	Glu	Thr	Glu	Asn	Arg	Leu	His	
				165					170					175		
Phe	Thr	Ile	Lys	Asp	Pro	Ala	Asn	Arg	Arg	Tyr	Glu	Val	Pro	Leu	Glu	
			180					185					190			
Thr	Pro	Arg	Val	His	Ser	Arg	Ala	Pro	Ser	Pro	Leu	Tyr	Ser	Val	Glu	
		195					200					205				
Phe	Ser	Glu	Glu	Pro	Phe	Gly	Val	Ile	Val	His	Arg	Gln	Leu	Asp	Gly	
	210					215					220					
Arg	Val	Leu	Leu	Asn	Thr	Thr	Val	Ala	Pro	Leu	Phe	Phe	Ala	Asp	Gln	
225					230					235					240	
Phe	Leu	Gln	Leu	Ser	Thr	Ser	Leu	Pro	Ser	Gln	Tyr	Ile	Thr	Gly	Leu	
				245					250					255		

Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile  
 260 265 270

Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr  
 275 280 285

Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His  
 290 295 300

Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro  
 305 310 315 320

Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr  
 325 330 335

Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp  
 340 345 350

Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His  
 355 360 365

Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val  
 370 375 380

Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn Asp  
 385 390 395 400

Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly  
 405 410 415

Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly Arg  
 420 425 430

Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala  
 435 440 445

Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile  
 450 455 460

Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser  
 465 470 475 480

Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu  
 485 490 495

Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Leu Trp  
 500 505 510

Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly  
 515 520 525

Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val  
 530 535 540

Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe  
 545 550 555 560

Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Pro  
 565 570 575

Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe  
 580 585 590

Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His  
 595 600 605

Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser Val  
 610 615 620

Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly Ala  
 625 630 635 640

Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg  
 645 650 655

Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn Ser  
 660 665 670

Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro Ala Gln  
 675 680 685

Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro His  
 690 695 700

Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly Glu Thr Val Ala  
 705 710 715 720

Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser Thr Trp Thr Val  
 725 730 735

Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val Leu  
 740 745 750

Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp  
 755 760 765

Tyr Asp Leu Gln Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro  
 770 775 780

Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp  
 785 790 795 800

Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala  
 805 810 815

Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser  
 820 825 830

Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu  
 835 840 845

Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val Leu  
 850 855 860

Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn Asn Thr  
 865 870 875 880

Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala Gly Leu Gln  
 885 890 895

Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln Val  
 900 905 910

Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr Ser Pro Asp Thr  
 915 920 925

Lys Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly Glu Gln Phe Leu  
 930 935 940

Val Ser Trp Cys  
 945

<210> 3  
 <211> 43  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic primer

<400> 3  
 gcgataggta ccgcatggg agtgaggcac ccgcctgct ccc

43

<210> 4  
 <211> 43  
 <212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 4

gcgatactcg agtcaacacc agctgacgag aaactgctct ccc

43